GOVERNMENT OF INDIA
HEALTH AND FAMILY WELFARE
LOK SABHA

UNSTARRED QUESTION NO:4236
ANSWERED ON:23.04.2008
BIRD FLU VIRUSES
Singh Kunwar Rewati Raman

Will the Minister of HEALTH AND FAMILY WELFARE be pleased to state:

(a) whether the different types of the viruses are likely to be generated by bird flu;

(b) if so, the details thereof;

(c) whether the scientists have reported the existence of the deadly Hanta Virus in the country for the first time;

(d) if so, the details thereof; and

(e) the action taken by the Government in this regard?

Answer

THE MINISTER OF HEALTH AND FAMILY WELFARE(DR. ANBUMANI RAMADOSS)

(a) & (b) Avian influenza A H5 and H7 viruses can be distinguished as "low pathogenic" and "high pathogenic" forms on the basis of genetic features of the virus and the severity of the illness they cause in poultry; influenza H9 virus has been identified only in a "low pathogenicity" form. Each of these three avian influenza A viruses (H5, H7, and H9) theoretically can be partnered with any one of nine neuraminidase surface proteins; thus, there are potentially nine different forms of each subtype (e.g. H5N1, H5N2, H5N3, H5N9).The virus causing alarm at present is H5N1 strain of the Influenza A virus.

(c) to (e) Indian Council of Medical Research is funding an extramural project entitled "Molecular and serological investigations of Hanta virus infections in Vellore district of south India" at Christian Medical College (CMC), Vellore.The ongoing study has been initiated in September,2006 Till date 360 health blood donors, 151 patients with chronic renal diseases, 99 members of the Irula tribe (occupational hazard) and 51 warehouse workers occupational hazard were tested. The irulas had a statistically significant seropositivity (11%) compared to healthy blood donors (4%) positive by two serological assays.In 6 (2.6%) human patients with acute febrile illness of 266 tested Polymerase Chain Reaction [PCR] was positive for hantavirus nucleic acid.The PCR products showed a 93-97% nucleotide homology with Hantaan virus (HTNV) on Phylogenetic analysis.The HTNV is most prevalent virus in South East Asia, China, Korea and Russia.There was no mortality among these hantavirus positive individuals.